

### IN THE CLAIMS

Please cancel claims 1 and 10.

Please amend claims 2 to 9, 11 to 20 to read as follows:

---

- A1
2. (Amended) A method according to claim 33 in which the first probability function is the probability that the defined type provides one or both of the mixture sources based on the frequency of occurrence of the possible allele combinations which could generate the identified allele identity or identities for that locus.
  3. (Amended) A method according to claim 33 in which the second probability function is the probability that the first and second other persons provide the identity for the mixture sources based on the frequency of occurrence of possible allele combinations which could have generated the identified allele identity or identities for that locus.
  4. (Amended) A method according to claim 33 where the defined type is the given person and an unknown person, the first function is based on the frequency of occurrence of the different possible allele combinations for the unknown person which are possible knowing the given persons alleles at that locus.
  5. (Amended) A method according to claim 33 where the defined type is the given person and an unknown person, the second function is based on the frequency of occurrence of the different allele combinations which are possible from the two unknown persons which give the allele identity or identities obtained.
  6. (Amended) A method according to claim 33 where the defined type is the given person and the first other person is a known person, the first function is defined as 1.
  7. (Amended) A method according to claim 33 where the defined type is the given person and the first other person is a known person, the second function is based on the

frequency of occurrence of the different possible allele combinations for the unknown person which are possible knowing the known person's alleles at that locus.

8. (Amended) A method according to claim 33 in which the method is applied to at least 20 loci.

9. (Amended) A method according to claim 33 in which the combined likelihood ratio is obtained by multiplying the individual likelihood ratios together.

AI 11. (Amended) A method according to claim 33 where the allele identity or identities of a given person and/or known first other person are under consideration, the method includes the determination of the allele identity or identities at one or more of the loci under consideration from DNA obtained only from the given person or known first person.

12. (Amended) A method according to claim 33 where the defined type is the given person and the first other person is a known person, such as a victim, and at least some of the loci considered in the method are those in which the given person and first other person are known to differ in allele identity.

13. (Amended) A method according to claim 33 where the defined type is the given person and the first other person is a known person, such as a victim, the method considers loci at which the given person and known first person are known to have the same homozygous allele identity.

14. (Amended) A method according to claim 33 in which in such cases the method includes the establishment of a probability value that the other identity is absent.

15. (Amended) A method according to claim 41 in which the probability value involves an investigation of the background noise level from the allele identity investigating process and / or the introduction of one or more negative control samples

and / or the determination of a cumulative probability density function for one or more or all of the negative controls.

16. (Amended) A method according to claim 41 where the defined type is the given person and the first other person is a known person, such as a victim, the method involves the establishment of a probability value that the given person's allele identity or identities has not been detected.

A1  
Concl  
17. (Amended) A method according to claim 41 in which the probability value relates to the given person's allele identity being different from that of the known first other person's.

18. (Amended) A method according to claim 41 in which the probability value relates to the given person's allele identity being the same as that of the known first other person's.

19. (Amended) A method according to claim 41 in which the method further includes the prediction of the proportion of the mixture arising from the person other than the first other person, for instance from the suspect as the given person.

20. (Amended) A method according to claim 41 in which the method includes an estimate or calculation of a value for  $p(\text{null})$ , the value for  $p(\text{null})$  being calculated from a cumulative probability density function.

---

Please add the following new claims, 21 to 41:

A2  
21. (New) A method for indicating the likelihood that a DNA mixture arose from sources of a defined type where the DNA mixture is formed by DNA samples from more than one source, the method involving:-

the determination of the identity of the single nucleotide polymorphism alleles present at a locus for the DNA in the mixture;

determining a first probability function for the situation where the mixture is formed from samples arising from the given person and from a first other person where the alleles identified have one or more of only two possible identities;

determining a second probability function for the situation where the DNA mixture is formed from samples arising from the second other person and a first other person where the alleles identified have one or both of only two possible identities;

using a first probability function as a numerator, and a second probability function as a denominator in determining a likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

determining such likelihood ratios for a plurality of single nucleotide polymorphism loci; and

combining the likelihood ratios to give a combined likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

and where the minimum number of loci needed to achieve a minimum combined likelihood ratio is calculated from

A2

$$\overline{LRn} = \prod_{m=1}^{mp} LR^{(f_m x n)}$$

where n is the number of loci; mp is the number of possible allele identities for a sample mixture; LR is the likelihood;  $\overline{LR}$  is the combined likelihood ratio; and fm is the frequency of occurrence of a particular mixture type m for a loci.

22. (New) A method according to claim 21 in which mp is 9.

23. (New) A method according to claim 21 in which the frequency of occurrence of a particular mixture type m for a loci is as stated in this claim in respect of the stated allele identities m:-

Mixture	AA,AA	AA,AB	AB,AA	AA,BB	BB,AA	AB,AB	AB,BB	BB,AB	BB,BB
---------	-------	-------	-------	-------	-------	-------	-------	-------	-------

type (m)									
Frequency (fm)	fa <sup>4</sup>	f2a <sup>3</sup> b	2a <sup>3</sup> b	fa <sup>2</sup> b <sup>2</sup>	fa <sup>2</sup> fb <sup>2</sup>	4fa <sup>2</sup> b <sup>2</sup>	2fafb <sup>3</sup>	2fafb <sup>3</sup>	fb <sup>4</sup>

24. (New) A method according to claim 21 in which the minimum combined likelihood ratio is  $1 \times 10^4$  or more.

25. (New) A method according to claim 21 in which the minimum combined likelihood ratio is  $1 \times 10^{16}$  or more.

26. (New) A method according to claim 21 where the allele identity or identities of a given person and/or known first other person are under consideration, the method includes the determination of the allele identity or identities at one or more of the loci under consideration from DNA obtained only from the given person or known first person.

27. (New) A method according to claim 21 where the defined type is the given person and the first other person is a known person, such as a victim, and at least some of the loci considered in the method are those in which the given person and first other person are known to differ in allele identity.

28. (New) A method of estimating the minimum number of loci to be used in a method for indicating the likelihood that a DNA mixture arose from sources of a defined type where the DNA mixture is formed by DNA samples from more than one source, the method of estimating including selecting a minimum combined likelihood ratio and calculating the number of loci needed according to a theoretical likelihood ratio calculated from:

$$\overline{LRn} = \prod_{m=1}^{mp} LR^{(fmxn)}$$

where  $n$  is the number of loci;  $m_p$  is the number of possible allele identities for a sample mixture;  $LR$  is the likelihood ratio;  $\overline{LR}$  is the combined likelihood ratio; and  $f_m$  is the frequency of occurrence of a particular mixture type  $m$  for a loci.

29. (New) A method according to claim 28 wherein  $m_p$  is 9.

30. (New) A method according to claim 28 in which the frequency of occurrence of a particular mixture type  $m$  for a loci is as started in this claim in respect of the stated allele identities  $m$ :-

A2

Mixture type (m)	AA,AA	AA,AB	AB,AA	AA,BB	BB,AA	AB,AB	AB,BB	BB,AB	BB,BB
Frequency (f <sub>m</sub> )	$f_n^4$	$f_2a^3b$	$2a^3b$	$fa^2b^2$	$fa^2fb^2$	$4fa^2b^2$	$2fafb^3$	$2fafb^3$	$fb^4$

31. (New) A method according to claim 28 in which the minimum combined likelihood ratio is  $1 \times 10^4$  or more.

32. (New) A method according to claim 28 in which the minimum combined likelihood ratio is  $1 \times 10^{16}$  or more.

33. (New) A method for indicating the likelihood that a DNA mixture arose from sources of a defined type where the DNA mixture is formed by DNA samples from more than one source the method involving:-

a determination of the identity of single nucleotide polymorphism alleles present at a locus in the DNA in the mixture;

determining a first probability function for a situation where the DNA mixture is formed from samples arising from a given person and from a first other person, where the alleles identified have one or both of only two possibilities;

determining a second probability function for a situation where the DNA mixture is formed from samples arising from a second other person and a first other person, where the alleles identified have one or both of only two possible identities;

using the first probability function as a numerator and the second probability function as a denominator in determining a likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

determining such likelihood ratios for a plurality of single nucleotide polymorphism loci; and

A2 combining the likelihood ratios to give a combined likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

the method including the establishment of a probability value that a person's allele identity or identities have not been detected which reflects the probability that the identity or identities is present but is not distinguished from the background noise.

34. (New) A method according to claim 33 in which the probability value relates to the given person's allele identity being different from that of the known first other person's.

35. (New) A method according to claim 36 in which the probability is expressed as a likelihood ratio and the likelihood ratio, when the first allele A and a second allele B are suggested for the profile and second allele B is not detected, is defined according to the equation:-

$$LR = \frac{p(B \neq \text{null})}{[2ab + b^2]p(B \neq \text{null}) + a^2 p(B = \text{null})}$$

where a and b are allele frequencies of first allele A and second allele B respectively, =null relates to allele B not being present, and ≠null relates to allele B being present but not distinguished from the background noise.

36. (New) A method according to claim 33 in which the probability value relates to the given person's allele identity being the same as that of the known first other person's.

37. (New) A method according to claim 36 in which the probability value is expressed as a likelihood ratio and the likelihood ratio, when a first allele A and a second allele A are suggested for the profile, and allele B is not detected, is defined according to the equation:-

$$LR = \frac{p(B = null)}{[2ab + b^2]p(B \neq null) + a^2 p(B = null)}$$

A2  
where a and b are allele frequencies of A and B respectively, =null relates to allele B not being present, and  $\neq$ null relates to allele B being present but not distinguished from the background noise.

38. (New) A method according to claim 33 in which the method further includes the prediction of the proportion of the mixture arising from the person other than the first other person, for instance from the suspect as the given person.

39. (New) A method according to claim 33 in which the method includes an estimate or calculation of a value for p(null), the value for p(null) being calculated from a cumulative probability density function.

40. (New) A method according to claim 33 in which the probability value involves an investigation of the background noise level from the allele identity investigating process and / or the introduction of one or more negative control samples and / or the determination of a cumulative probability density function for one or more or all of the negative controls.



41. (New) A method for indicating the likelihood that a DNA mixture arose from sources of a defined type where the DNA mixture is formed by DNA samples from more than one source, the method involving:-

a determination of the identity of the single nucleotide polymorphism alleles present at a locus in the DNA in the mixture;

determining a first probability function for the situation where the DNA mixture is formed from samples arising from the given person and from a first other person, where the alleles identified have one or both of only two possibilities;

determining a second probability function for the situation where the DNA mixture is formed from samples arising from a second other person and a first other person, where the alleles identified have one or both of only two possible identities;

using the first probability function as a numerator and the second probability function as a denominator in determining a likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

determining such likelihood ratios for a plurality of single nucleotide polymorphism loci; and

combining the likelihood ratios to give a combined likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

where the defined type is the given person and the first other person is a known person, such as a victim, the method considers loci at which the given person and known first person are known to have the same homozygous allele identity and the method provides the establishment of a probability value that a person's allele identity or identities have not been detected which reflects the probability that the identity or identities is absent, rather than present but not detected.